

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastp suite-2sequences/ Formatting Results - NBR3PYEF112

Blast 2 sequences

alignment of GenBank Prot ID 3193318 and claimed SEQ ID NO: 2

Query ID	gi 10177290 dbj BAB10551.1	Subject ID	32133
Description	unnamed protein product [Arabidopsis thaliana]	Description	None
Molecule type	amino acid	Molecule type	amino acid
Query Length	186	Subject Length	228
		Program	BLASTP 2.2.25+

[Dot Matrix View](#)

Plot of gi|10177290|dbj|BAB10551.1| vs 32133 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [P](#) PubChem BioAssay

Accession	Description	Max score	Total score	Query coverage	E value	Links
32133	unnamed protein product 127	127	84%	1e-34		

Alignments

>lcl|32133 unnamed protein product
Length=228

Score = 127 bits (319), Expect = 1e-34, Method: Compositional matrix adjust.
Identities = 78/167 (47%), Positives = 96/167 (58%), Gaps = 11/167 (6%)

Query	14	ACKFLRRKCMGCFAPYFPPEE-PHKFANVHKIFGASNVTKLLNELLPHQREDAVNSLA	72
Sbjct	20	ACKFLRRKC+ GCIFAPYF E+ FA VHK+FGASNV+KLL+ + H+R DAV S+	79
Query	73	YEAEARVRDPVYGCVGAISYLRQVHRLQKELDAANADLAHYGLSTSAAGAPGNVVDLVF	132
Sbjct	80	FEAQRALRDPYIGCVSHIVSLQQQVVSLQTELSYLAHLATLELPQPQPVPVSSSGSL	139
Query	133	QQOPLSPQLPLPNP-VYRLSGA-SPVMN-----QMPRGTTGSSYGT	171
Sbjct	140	Q L LP ++P VY LS PVM+ Q PR + +G	184